

PCT10

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,852

DATE: 01/14/2002

TIME: 07:37:21

Input Set : A:\REG710AUS3.txt

Output Set: N:\CRF3\01142002\J009852.raw

**ENTERED**

4 <110> APPLICANT: Nicholas J. Papadopoulos et al.  
6 <120> TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED  
7 PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING  
8 AND USING THEREOF  
10 <130> FILE REFERENCE: REG 710-A-US  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/009,852  
C--> 13 <141> CURRENT FILING DATE: 2001-12-06  
15 <150> PRIOR APPLICATION NUMBER: PCT/US00/14142  
16 <151> PRIOR FILING DATE: 2000-05-23  
18 <150> PRIOR APPLICATION NUMBER: 60/138,133  
19 <151> PRIOR FILING DATE: 1999-06-08  
21 <160> NUMBER OF SEQ ID NOS: 38  
23 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
25 <210> SEQ ID NO: 1  
26 <211> LENGTH: 1704  
27 <212> TYPE: DNA  
28 <213> ORGANISM: Homo sapiens  
30 <220> FEATURE:  
31 <221> NAME/KEY: CDS  
32 <222> LOCATION: (1)...(1701)  
34 <400> SEQUENCE: 1

35	atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg ctc agc	48
36	Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser	
37	1 5 10 15	
39	tgt ctg ctt ctc aca gga tct agt tca ggt tca aaa tta aaa gat cct	96
40	Cys Leu Leu Leu Thr Gly Ser Ser Gly Ser Lys Leu Lys Asp Pro	
41	20 25 30	
43	gaa ctg agt tta aaa ggc acc cag cac atc atg caa gca ggc cag aca	144
44	Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr	
45	35 40 45	
47	ctg cat ctc caa tgc agg ggg gaa gca gcc cat aaa tgg tct ttg cct	192
48	Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro	
49	50 55 60	
51	gaa atg gtg agt aag gaa agc gaa agg ctg agc ata act aaa tct gcc	240
52	Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala	
53	65 70 75 80	
55	tgt gga aga aat ggc aaa caa ttc tgc agt act tta acc ttg aac aca	288
56	Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr	
57	85 90 95	
59	gct caa gca aac cac act ggc ttc tac agc tgc aaa tat cta gct gta	336
60	Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val	
61	100 105 110	
63	cct act tca aag aag aag gaa aca gaa tct gca atc tat ata ttt att	384
64	Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile	
65	115 120 125	
67	agt gat aca ggt aga cct ttc gta gag atg tac agt gaa atc ccc gaa	432
68	Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu	

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69	130	135	140	
71	att ata cac atg act gaa gga agg gag ctc gtc att ccc tgc cgg gtt	480		
72	Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val			
73	145 150 155 160			
75	acg tca cct aac atc act gtt act tta aaa aag ttt cca ctt gac act	528		
76	Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr			
77	165 170 175			
79	ttg atc cct gat gga aaa cgc ata atc tgg gac agt aga aag ggc ttc	576		
80	Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe			
81	180 185 190			
83	atc ata tca aat gca acg tac aaa gaa ata ggg ctt ctg acc tgt gaa	624		
84	Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu			
85	195 200 205			
87	gca aca gtc aat ggg cat ttg tat aag aca aac tat ctc aca cat cga	672		
88	Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg			
89	210 215 220			
91	caa acc aat aca atc ata gat gtc caa ata agc aca cca cgc cca gtc	720		
92	Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val			
93	225 230 235 240			
95	aaa tta ctt aga ggc cat act ctt gtc ctc aat tgt act gct acc act	768		
96	Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr			
97	245 250 255			
99	ccc ttg aac acg aga gtt caa atg acc tgg agt tac cct gat gaa aaa	816		
100	Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys			
101	260 265 270			
103	aat aag aga gct tcc gta agg cga cga att gac caa agc aat tcc cat	864		
104	Asn Lys Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His			
105	275 280 285			
107	gcc aac ata ttc tac agt gtt ctt act att gac aaa atg cag aac aaa	912		
108	Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys			
109	290 295 300			
111	gac aaa gga ctt tat act tgt cgt gta agg agt gga cca tca ttc aaa	960		
112	Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys			
113	305 310 315 320			
115	tct gtt aac acc tca gtg cat ata tat gat aaa gca ggc ccg ggc gag	1008		
116	Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu			
117	325 330 335			
119	ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct	1056		
120	Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro			
121	340 345 350			
123	gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag	1104		
124	Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys			
125	355 360 365			
127	gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg	1152		
128	Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val			
129	370 375 380			
131	gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac	1200		
132	Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp			
133	385 390 395 400			

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135 ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac      1248
136 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
137          405                      410                      415
139 aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac      1296
140 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
141          420                      425                      430
143 tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc      1344
144 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
145          435                      440                      445
147 cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga      1392
148 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
149          450                      455                      460
151 gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag      1440
152 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
153          465                      470                      475                      480
155 aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac      1488
156 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
157          485                      490                      495
159 atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag      1536
160 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
161          500                      505                      510
163 acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc      1584
164 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
165          515                      520                      525
167 aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca      1632
168 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
169          530                      535                      540
171 tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc      1680
172 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
173          545                      550                      555                      560
175 ctc tcc ctg tct ccg ggt aaa tga
176 Leu Ser Leu Ser Pro Gly Lys      1704
177          565
180 <210> SEQ ID NO: 2
181 <211> LENGTH: 567
182 <212> TYPE: PRT
183 <213> ORGANISM: Homo sapiens
185 <400> SEQUENCE: 2
186 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
187 1          5          10          15
188 Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
189          20          25          30
190 Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
191          35          40          45
192 Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
193          50          55          60
194 Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
195          65          70          75          80
196 Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr

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197          85          90          95
198 Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
199          100          105          110
200 Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
201          115          120          125
202 Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
203          130          135          140
204 Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
205          145          150          155          160
206 Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
207          165          170          175
208 Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
209          180          185          190
210 Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu
211          195          200          205
212 Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
213          210          215          220
214 Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val
215          225          230          235          240
216 Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr
217          245          250          255
218 Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys
219          260          265          270
220 Asn Lys Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His
221          275          280          285
222 Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys
223          290          295          300
224 Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys
225          305          310          315          320
226 Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu
227          325          330          335
228 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
229          340          345          350
230 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
231          355          360          365
232 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
233          370          375          380
234 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
235          385          390          395          400
236 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
237          405          410          415
238 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
239          420          425          430
240 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
241          435          440          445
242 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
243          450          455          460
244 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
245          465          470          475          480

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```

246 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
247                               485                               490                               495
248 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
249                               500                               505                               510
250 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
251                               515                               520                               525
252 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
253                               530                               535                               540
254 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
255                               545                               550                               555                               560
256 Leu Ser Leu Ser Pro Gly Lys
257                               565
259 <210> SEQ ID NO: 3
260 <211> LENGTH: 1674
261 <212> TYPE: DNA
262 <213> ORGANISM: Homo sapiens
264 <220> FEATURE:
265 <221> NAME/KEY: CDS
266 <222> LOCATION: (1)...(1671)
268 <400> SEQUENCE: 3
269 atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg ctc agc
270 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
271 1 5 10 15
273 tgt ctg ctt ctc aca gga tct agt tca ggt tca aaa tta aaa gat cct
274 Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
275 20 25 30
277 gaa ctg agt tta aaa ggc acc cag cac atc atg caa gca ggc cag aca
278 Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
279 35 40 45
281 ctg cat ctc caa tgc agg ggg gaa gca gcc cat aaa tgg tct ttg cct
282 Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
283 50 55 60
285 gaa atg gtg agt aag gaa agc gaa agg ctg agc ata act aaa tct gcc
286 Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
287 65 70 75 80
289 tgt gga aga aat ggc aaa caa ttc tgc agt act tta acc ttg aac aca
290 Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
291 85 90 95
293 gct caa gca aac cac act ggc ttc tac agc tgc aaa tat cta gct gta
294 Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
295 100 105 110
297 cct act tca aag aag aag gaa aca gaa tct gca atc tat ata ttt att
298 Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
299 115 120 125
301 agt gat aca ggt aga cct ttc gta gag atg tac agt gaa atc ccc gaa
302 Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
303 130 135 140
305 att ata cac atg act gaa gga agg gag ctc gtc att ccc tgc cgg gtt
306 Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val

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## VERIFICATION SUMMARY

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Input Set : A:\REG710AUS3.txt

Output Set: N:\CRF3\01142002\J009852.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date